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SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> A gene encoding an enzyme for catalyzing biosynthesis of lignan,
and use thereof

<130> SU0411

<140> PCT/JP2004/0146696

<141> 2004-09-24

<150> JP 2003-341313

<151> 2003-09-30

<150> JP 2003-432383

<151> 2003-12-26

<160> 79

<170> PatentIn Ver. 2.1

<210> 1

<211> 506

<212> PRT

<213> Sesamum indicum

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Val	Ala	Ala	Lys	Arg	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Asp	Glu	Glu	195	200	205	
Ala	Lys	Arg	Phe	Arg	Asp	Leu	Thr	Lys	Glu	Ala	Leu	Glu	Leu	Thr	Ser	210	215	220	
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<210> 13

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<210> 14

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<210> 16

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 Synthesized Primer Sequence, CYP705A-RV

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Synthesized Primer Sequence, CYP83A-RV

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Synthesized Primer Sequence, SiP168-FW

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 <400> 36
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Ala	Leu	Ser	Leu	Ser	Ser	Arg	Met	Ile	Ser	Arg	Phe	Ala	Leu	Gly	Lys
			180					185					190		
Arg	Tyr	Asp	Glu	Glu	Asn	Gly	Pro	Glu	Lys	Arg	Arg	Phe	Asp	Arg	Ile
		195					200					205			
Leu	Gln	Leu	Leu	Gln	Leu	Val	Ser	Val	Glu	Ile	Phe	Phe	Gly	Asp	Tyr
	210					215					220				
Ser	Pro	Trp	Leu	Gly	Trp	Ile	Asp	Arg	Leu	Cys	Gly	Lys	Val	Ser	Gln
225					230					235					240
Leu	Glu	Lys	Ala	Phe	Lys	Asp	Leu	Asp	Ser	Leu	Tyr	Glu	Glu	Met	Ile
				245					250					255	
Ala	Glu	His	Leu	Ser	Pro	Asn	Arg	Pro	Glu	Ser	Met	Asn	Gly	Asp	Ile
			260					265					270		

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln
 275 280 285
 Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala
 290 295 300
 Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu
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 Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser
 325 330 335
 Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu
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 Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro
 355 360 365
 Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp
 370 375 380
 Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala
 385 390 395 400
 Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro
 405 410 415
 Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly
 420 425 430
 Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu
 435 440 445
 Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe
 450 455 460
 His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp
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 Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met
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 Ala Lys Ser Tyr Leu
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<211> 1545

<212> DNA

<213> Sesamum indicum

<220>

<223> SiP288

<400> 55

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gatcctgaga atgttccacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300
aagttcaggg aaatttttga tgttcttggg gatgggattt tcaatgcaga ttcggagtcc 360
tggaggggacc agagaagggg tgccagggcc ctgatttctc accatgggtt cctccgggtt 420
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<210> 56

<211> 515

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP288

<400> 56

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  1               5               10               15

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Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp
      20               25               30

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Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile
      35               40               45

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His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe
      50               55               60

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His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala
      65               70               75               80

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Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe
      85               90               95

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Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly
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Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala

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145					150					155					160	
Cys	Leu	Glu	Asn	Arg	Val	Val	Asp	Leu	Gln	Asp	Leu	Phe	Gln	Arg	Leu	
165					170					175						
Thr	Phe	Asp	Thr	Thr	Cys	Thr	Phe	Val	Thr	Gly	Tyr	Asp	Pro	Gly	Cys	
180					185					190						
Leu	Ser	Val	Asp	Leu	Pro	Asp	Val	Pro	Phe	Ser	Lys	Ala	Leu	Asp	Asp	
195					200					205						
Ala	Glu	Glu	Ala	Ile	Phe	Met	Arg	His	Val	Val	Pro	Glu	Lys	Ile	Trp	
210					215					220						
Lys	Leu	Gln	Arg	Trp	Phe	Gly	Val	Gly	Ser	Glu	Arg	Lys	Leu	Ser	Lys	
225					230					235					240	
Ala	Arg	Glu	Val	Leu	Asp	Ser	Val	Ile	Gly	Arg	Tyr	Ile	Ala	Leu	Lys	
245					250					255						
Arg	Gly	Glu	Met	Arg	Ser	Arg	Gly	Ile	Ser	Ile	Asp	Cys	Glu	Asn	Glu	
260					265					270						
Asp	Gly	Val	Asp	Leu	Leu	Thr	Ser	Tyr	Met	Thr	Val	Gly	Asp	Asp	Gly	
275					280					285						
Thr	Gln	Thr	His	Asp	Leu	Lys	Cys	Asp	Asp	Lys	Phe	Leu	Arg	Asp	Thr	
290					295					300						
Ile	Leu	Asn	Leu	Met	Ile	Ala	Gly	Arg	Asp	Thr	Thr	Ser	Ser	Ala	Leu	
305					310					315					320	
Thr	Trp	Phe	Ile	Trp	Leu	Val	Ser	Thr	His	Ala	Glu	Val	Glu	Lys	Arg	
325					330					335						
Ile	Arg	Asp	Glu	Leu	Lys	Ser	Phe	Leu	Pro	Ala	Gly	Glu	Arg	Glu	Lys	
340					345					350						
Trp	Arg	Val	Phe	Gly	Val	Glu	Glu	Thr	Lys	Lys	Leu	Val	Tyr	Met	His	
355					360					365						
Gly	Ala	Ile	Cys	Glu	Ala	Leu	Arg	Leu	Tyr	Pro	Pro	Val	Pro	Phe	Gln	
370					375					380						
His	Lys	Glu	Pro	Val	Glu	Pro	Asp	Ile	Leu	Pro	Ser	Gly	His	Phe	Val	
385					390					395					400	
Glu	Pro	Thr	Met	Lys	Val	Met	Phe	Ser	Leu	Tyr	Ala	Met	Gly	Arg	Met	
405					410					415						
Glu	Ser	Val	Trp	Gly	Glu	Asp	Cys	Leu	Glu	Phe	Lys	Pro	Glu	Arg	Trp	

420	425	430
Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu		
435	440	445
Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe		
450	455	460
Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val		
465	470	475
His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu		
485	490	495
Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala		
500	505	510

Lys Lys Asn
515

<210> 57
 <211> 1494
 <212> DNA
 <213> Sesamum indicum

<220>
 <223> SiP168

<400> 57

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gccaaactct	ccaaaaccta	cggggccctg	atgcgtctca	agctgggaac	catgacaaca	240
gttggttgat	cctccccgga	aatctccagg	atcgtgctgc	aacaatatga	ccaagttttc	300
tccagccgaa	cacacgcaga	tgccatccga	gcacttgacc	accacaaaca	ttccgtcgcc	360
tggataccgg	cggacaatca	gtggcggaaa	atccgtaaac	tgtgcaaaga	gaagatgttt	420
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<212> PRT
<213> Sesamum indicum

<220>
<223> SiP168

<400> 58

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			20					25					30		
Ser	Ala	Asn	Leu	Pro	Pro	Gly	Pro	Lys	Pro	Leu	Pro	Ile	Ile	Gly	Asn
		35					40					45			
Ile	Leu	Glu	Leu	Gly	Glu	Lys	Pro	His	Gln	Ser	Leu	Ala	Lys	Leu	Ser
	50					55					60				
Lys	Thr	Tyr	Gly	Pro	Leu	Met	Arg	Leu	Lys	Leu	Gly	Thr	Met	Thr	Thr
65					70				75						80
Val	Val	Val	Ser	Ser	Pro	Glu	Ile	Ser	Arg	Ile	Val	Leu	Gln	Gln	Tyr
				85					90					95	
Asp	Gln	Val	Phe	Ser	Ser	Arg	Thr	His	Ala	Asp	Ala	Ile	Arg	Ala	Leu
		100						105					110		
Asp	His	His	Lys	His	Ser	Val	Ala	Trp	Ile	Pro	Ala	Asp	Asn	Gln	Trp
	115						120					125			
Arg	Lys	Ile	Arg	Lys	Leu	Cys	Lys	Glu	Lys	Met	Phe	Ser	Gly	Gln	Lys
	130					135					140				
Leu	Asp	Ala	Asn	Gln	Gly	Leu	Arg	Arg	Glu	Lys	Leu	Arg	Asn	Leu	Gln
145					150					155					160
Asp	Tyr	Val	Asn	Glu	Cys	Cys	Val	Ser	Gly	Gln	Val	Val	Asp	Ile	Gly
				165					170					175	
Val	Ala	Ala	Phe	Thr	Thr	Thr	Leu	Asn	Leu	Ile	Ser	Ala	Thr	Leu	Phe
			180					185					190		
Ser	Val	Asp	Phe	Ala	Asp	Phe	Gly	Ser	Gly	Ser	Ser	Gln	Glu	Leu	Lys
		195					200					205			
Asp	Val	Met	Ser	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Arg	Pro	Asn	Phe	Ala
	210					215					220				
Asp	Cys	Phe	Pro	Leu	Leu	Arg	Leu	Val	Asp	Pro	Gln	Gly	Ile	Phe	Arg
225					230				235						240
Gln	Thr	Thr	Leu	His	Phe	Asn	Lys	Cys	Phe	Lys	Ile	Phe	Asp	Glu	Ile
				245					250					255	

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met
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 275 280 285
 Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr
 290 295 300
 Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg
 305 310 315 320
 His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val
 325 330 335
 Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr
 340 345 350
 Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro
 355 360 365
 Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr
 370 375 380
 Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly
 385 390 395 400
 Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg
 405 410 415
 Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu
 420 425 430
 Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr
 435 440 445
 Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp
 450 455 460
 Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys
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 Lys Ile

<210> 59
 <211> 1545
 <212> DNA
 <213> Sesamum indicum

<220>
 <223> SiP236


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ctaagtgatg aaagaaagac agtaaaactac agaccaatgc tcactcttct catcgacggt 1500
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<210> 60
<211> 515
<212> PRT
<213> Sesamum indicum

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<220>
<223> SiP236

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      20             25             30

Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr
      35             40             45

Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala
      50             55             60

Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg
      65             70             75             80

Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys
      85             90             95

Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu

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100					105					110					
Gly	Asp	Leu	Phe	Gly	Glu	Gly	Ile	Phe	Ala	Ile	Asp	Gly	His	Lys	Trp
	115						120					125			
Arg	Glu	Gln	Arg	Lys	Val	Ser	Ser	Leu	Glu	Phe	Ser	Thr	Arg	Val	Leu
	130					135					140				
Arg	Asp	Tyr	Ser	Ser	Ile	Val	Phe	Arg	Lys	Asn	Ala	Val	Arg	Leu	Ala
	145					150					155				160
Lys	Ile	Leu	Ser	Gly	Ala	Ala	Thr	Ser	Asn	Gln	Pro	Val	Asp	Ile	Gln
				165					170					175	
Asp	Leu	Phe	Met	Lys	Ser	Thr	Phe	Asp	Ser	Ile	Ser	Glu	Val	Ala	Leu
			180					185					190		
Gly	Val	Glu	Leu	Asp	Ser	Leu	Gly	Gly	Ser	Asn	Glu	Glu	Gly	Ala	Lys
		195					200					205			
Phe	Ser	Ile	Ala	Ala	Asp	Asp	Val	Ser	Met	Arg	Thr	Leu	Trp	Arg	Tyr
	210					215					220				
Val	Asp	Val	Leu	Trp	Lys	Leu	Lys	Arg	Ala	Leu	Asn	Val	Gly	Ser	Glu
	225					230					235				240
Ala	Lys	Leu	Lys	Lys	Ser	Leu	Gln	Val	Val	Asp	Glu	Phe	Val	Tyr	Lys
			245						250					255	
Leu	Ile	His	Ser	Arg	Thr	Gln	Gln	Met	Asn	Met	Pro	Gly	Asn	Asp	Ser
			260					265					270		
Val	Met	Gln	Leu	Lys	Lys	Asp	Asp	Ile	Leu	Ser	Arg	Phe	Leu	Gln	Leu
	275						280					285			
Thr	Glu	Ala	Thr	Pro	Lys	Tyr	Leu	Arg	Asp	Ile	Thr	Ile	Ser	Phe	Ile
	290					295					300				
Val	Ala	Gly	Lys	Asp	Thr	Thr	Ala	Thr	Thr	Leu	Ser	Trp	Phe	Ile	Tyr
	305					310					315				320
Met	Leu	Cys	Lys	Tyr	Pro	His	Val	Gln	Glu	Lys	Val	Glu	Gln	Glu	Ile
			325						330					335	
Lys	Asp	Ala	Thr	Gly	Cys	Lys	Glu	Val	Ala	Asp	Ile	Ser	Glu	Phe	Ser
		340						345					350		
Ala	Cys	Val	Thr	Glu	Glu	Ala	Leu	Gly	Lys	Met	His	Tyr	Leu	His	Ala
		355					360					365			
Ala	Leu	Thr	Glu	Thr	Leu	Arg	Ile	Tyr	Pro	Ala	Val	Ala	Val	Asp	Ala
	370					375					380				
Lys	Gln	Cys	Leu	Cys	Asp	Asp	Ile	Met	Pro	Asp	Gly	Phe	Ser	Val	Lys
	385					390					395				400
Lys	Gly	Asp	Met	Val	Ala	Tyr	Gln	Pro	Tyr	Ala	Met	Gly	Arg	Met	Lys

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Ser Ile Trp Gly Asn Asp Ala Glu Glu Phe Lys Pro Glu Arg Trp Leu		
420	425	430
Asp Lys Asn Gly Cys Phe Gln Gln Ala Ser Pro Phe Lys Phe Thr Ala		
435	440	445
Phe Gln Ala Gly Pro Arg Leu Cys Leu Gly Lys Glu Phe Ala Tyr Arg		
450	455	460
Gln Met Lys Ile Phe Ser Ala Ile Leu Leu Arg Phe Phe Thr Met Lys		
465	470	475
Leu Ser Asp Glu Arg Lys Thr Val Asn Tyr Arg Pro Met Leu Thr Leu		
485	490	495
Leu Ile Asp Gly Gly Leu Ile Val Arg Pro Phe His Arg Met Asp Glu		
500	505	510
Lys Thr Ala		
515		

<210> 61
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, Bam-SST-FW2

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34

<210> 62
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, SiP189-Nco-RV

<400> 62
 gcaaatgatc aaccatggtg ttct

24

<210> 63
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, GR-SST-RV1

<400> 63

cacatgaacg agacgaactg ggttttgg

27

<210> 64

<211> 506

<212> PRT

<213> Sesamum radiatum

<220>

<223> SrSiP189

<400> 64

Met	Glu	Ala	Glu	Met	Leu	Tyr	Ser	Ala	Leu	Ala	Leu	Thr	Phe	Ala	Ile
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Phe	Met	Val	Tyr	Arg	Ile	Leu	Ser	Asn	Ser	Gln	Glu	Lys	Ser	Ser	Leu
			20					25					30		
Ile	Lys	Leu	Pro	Pro	Ser	Pro	Pro	Gly	Trp	Leu	Pro	Val	Ile	Gly	His
		35					40					45			
Val	His	Leu	Met	Lys	Asn	Leu	Leu	His	Arg	Thr	Leu	Tyr	Asp	Phe	Ser
	50					55					60				
Gln	Lys	Leu	Gly	Pro	Ile	Phe	Ser	Leu	Arg	Phe	Gly	Thr	Arg	Leu	Val
65					70					75					80
Val	Val	Val	Ser	Ser	Ser	Ser	Leu	Val	Glu	Glu	Cys	Phe	Thr	Lys	Tyr
			85						90					95	
Asp	Ile	Val	Leu	Ala	Asn	Arg	Pro	Gln	Pro	Ser	Val	Asp	Arg	Arg	Ser
		100						105					110		
Leu	Gly	Phe	Ser	Thr	Thr	Ser	Val	Ile	Gly	Ala	Pro	Tyr	Gly	Asp	His
	115						120					125			
Trp	Arg	Asn	Leu	Arg	Lys	Leu	Cys	Asp	Leu	Glu	Val	Phe	Ala	Pro	Thr
	130					135					140				
Arg	Leu	Ala	Ser	Phe	Leu	Ser	Ile	Arg	Leu	Asp	Glu	Arg	Asp	Arg	Met
145					150					155					160
Ile	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Ser	Ala	Gly	Phe	Ala	Lys	Val	Asn
			165						170					175	
Leu	Glu	Thr	Lys	Ile	Val	Glu	Leu	Thr	Phe	Asn	Asn	Ile	Met	Arg	Met
		180						185					190		
Val	Ala	Gly	Lys	Arg	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Asp	Glu	Glu
	195						200					205			

Ala	Lys	Arg	Phe	Arg	Asp	Leu	Thr	Lys	Glu	Ala	Leu	Glu	Leu	Thr	Ser	210	215	220	
Ala	Ser	Asn	Pro	Gly	Glu	Ile	Phe	Pro	Ile	Leu	Arg	Trp	Leu	Gly	Phe	225	230	235	240
Asn	Gly	Leu	Glu	Lys	Lys	Leu	Ala	Val	His	Ala	Arg	Lys	Thr	Asp	Glu	245	250	255	
Phe	Met	Gln	Gly	Leu	Leu	Asp	Glu	His	Arg	Arg	Gly	Glu	Arg	Gln	Asn	260	265	270	
Thr	Met	Val	Asp	His	Leu	Leu	Ser	Leu	Gln	Glu	Ser	Gln	Pro	Glu	Tyr	275	280	285	
Tyr	Thr	Asp	Glu	Ile	Ile	Thr	Gly	Leu	Ile	Val	Ala	Leu	Ile	Ile	Ala	290	295	300	
Gly	Thr	Asp	Ala	Ser	Val	Val	Thr	Thr	Glu	Trp	Ala	Met	Ser	Leu	Ile	305	310	315	320
Leu	Asn	His	Pro	Gln	Val	Leu	Glu	Lys	Ala	Arg	Lys	Glu	Leu	Asp	Thr	325	330	335	
Leu	Val	Gly	His	Glu	Arg	Met	Val	Asp	Glu	His	Asp	Leu	Pro	Lys	Leu	340	345	350	
Arg	Tyr	Leu	His	Cys	Ile	Val	Leu	Glu	Thr	Leu	Arg	Leu	Phe	Pro	Ser	355	360	365	
Val	Pro	Thr	Leu	Val	Pro	His	Glu	Pro	Ser	Glu	Asp	Cys	Lys	Ile	Gly	370	375	380	
Gly	Tyr	Asn	Val	Pro	Lys	Gly	Thr	Met	Ile	Leu	Val	Asn	Ala	Trp	Ala	385	390	395	400
Ile	His	Arg	Asp	Pro	Lys	Val	Trp	Asp	Asp	Pro	Leu	Ser	Phe	Lys	Pro	405	410	415	
Asp	Arg	Phe	Glu	Thr	Met	Glu	Val	Glu	Thr	His	Lys	Leu	Leu	Pro	Phe	420	425	430	
Gly	Met	Gly	Arg	Arg	Ala	Cys	Pro	Gly	Ala	Gly	Leu	Ala	Gln	Lys	Phe	435	440	445	
Val	Gly	Leu	Ala	Leu	Gly	Ser	Leu	Ile	Gln	Cys	Phe	Glu	Trp	Glu	Arg	450	455	460	
Met	Ser	Ala	Glu	Lys	Ile	Asp	Leu	Asn	Glu	Gly	Ser	Gly	Ile	Thr	Leu	465	470	475	480
Pro	Lys	Ala	Lys	Thr	Leu	Glu	Ala	Met	Cys	Lys	Pro	Arg	His	Ile	Met	485	490	495	
Glu	Arg	Val	Leu	Arg	Gln	Val	Ser	Asn	Val							500	505		

<210> 65
 <211> 1518
 <212> DNA
 <213> *Sesamum radiatum*

<220>
 <223> SrSiP189

<400> 65
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 agaattcttt ctaattcgca ggagaaaagc agcctgatta agctgccgcc gagcccgccg 120
 gggttggtcc cggatgatcg ccacgttcat ctcatgaaaa atctcctcca tagaacacta 180
 tacgacttct cccagaaact gggaccata tttccctcc gggtcgccac ccgcctcgtg 240
 gtagtgggtg cctcctcctc cctgggtcgag gaatgtttca ccaagtacga cattgtcttg 300
 gccaacgcc ctcagccctc tgtcgaccgg cgctcactcg gggtcagcac caccagcgta 360
 atcggcgccc cgtacgggga ccattggcgc aacctgcgaa agttgtgcga tcttgaagta 420
 ttgcctccga cccgtctcgc ctggttttta tccatcaggc ttgacgagag ggaccgcatg 480
 atttcgtcgt tgtacaaaat ctgctcggcc gggttcgcga aggtgaattt ggagacgaag 540
 attgttgagc tgacgtttta taacataatg aggatggtgg cggggaagag atactatggg 600
 gaggaggcgg aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660
 gagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggtttc 720
 aatgggttgg agaagaagct ggctgttcac gcgcggaaga cggatgagtt catgcaaggg 780
 ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca tttgctttcg 840
 ttgcaggaat ctcaacctga gtactacact gatgaaatca tctactggcct catagtgtgca 900
 ttgataattg cgggaacgga tgcacgggtt gtaactacag aatgggcgat gtcccttata 960
 ctaaactcct cccaagtact tgaaaaggct agaaaagaac tggacactct agtaggacac 1020
 gaacgcattg tcgatgaaca tgatctgccc aaactacgtt accttactg catagtcttg 1080
 gagaccttaa gggtattttc ttctgttcca acgttggtgc cacacgaacc atcggaggat 1140
 tgtaaaattg ggggatacaa tgtccccaag gggacaatga tactggtgaa tgcttgggca 1200
 atacaccgag accccaaggt gtgggacgac ccttgagct ttaagcccga caggtttgag 1260
 acaatggaag tggagacaca caagctgttg ccgttcggga tgggcaggag agcgtgtccc 1320
 ggagctggat tggcgagaa gtttgtgggg ttggctttgg ggctcgctgat tcagtgtttc 1380
 gagtgggaga gaatgagtg ggagaaaatt gacttgaacg aaggttctgg gataaccttg 1440
 cctaaagcta agacgttgga agccatgtgc aaacctagac atatcatgga gagagtctct 1500
 cgtcaggttt cgaacgct 1518

<210> 66
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, NtUBQ-FW

<400> 66
 ggaatgcaga tcttcgtcaa

20

<210> 67
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, NtUBQ-RW

<400> 67
 cctagaaacc accacgga 18

<210> 68
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, SiP189-bam-FW

<400> 68
 ttttcagcca acatggaagc tgaa 24

<210> 69
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, SiP189-nco-RV

<400> 69
 gcaaagatc aaccatggtg ttct 24

<210> 70
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, STAR-LF1

<400> 70
 acgaagttat gcggccaatt aaccc 25

<210> 71
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence, STAR-LR1

<400> 71
ccacctgacg tcgcggccta atacg 25

<210> 72
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, M13-47(F)

<400> 72
cgccaggggtt ttcccagtcg cgac 24

<210> 73
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, RV-M(R)

<400> 73
gagcggataa caatttcaca cagg 24

<210> 74
<211> 3069
<212> DNA
<213> Sesamun indium

<400> 74
tacgtggttg taaattaagg tggcatagtc aaagctgtgt aggatggagg aattagacac 60
ttccccagtc cccacagac tattcccgag ctgaccaa acagtcgaaa gtgtggggcc 120
caatgaaatt gacagatgac gtctagtgtg gtgtgaatgt gtgatatttt tgcagaatat 180
tgtaaaagag gggtcaccaa atctcactag tttgtgacta attgactatt tttgcagaaa 240
attcgtatatt agtatagggt cttgggtcaaa ttaattaatt atataacaaa tgtgatatat 300
ttaatttggtt attaatTTTT ttatatTTgt tgtgtaatta gttaggattt tatataagaa 360
tttgaaaaaa tgagatgttt ttttgtaaat caaattacac aatatcatgt attgggtttt 420
tcgtcctgaa gtcgcttgaa aattgattag atcggcggac ttgaacagac gagtgaatgg 480
acatgattta aaattttaag gataaatata tatagtatca gttatcaaaa taaaaaattt 540
ccttcaaaat catggtcttg ttttaagatag ttttttgagt aatgtggcac cataattccc 600
aagcactaga agtgcaattg taaatccaac ggtacctagt ttaattgata aaattaaagt 660
ccaaaaattt tcttgagaaa ccaattcgag caaggggtaca tcaaagggtgc caccagggag 720
ttaagcaaga aatgtccctt aaacttttag catgaggtat ccctataaaa taaattgacc 780
taaaaagatt caaatggctt agagtcgaga aaaagactaa gtagaccatt aggggaagccc 840
acatgcctaa gatcctccag ccgaagtaga ggcctatgag gcagtcagcc tagtgacttg 900
ggattcccta gctctgaaag aattaatatt gtcccaagaa tctaaggcta catagtagaa 960
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gaaagctggc caagaattat accttttaaa gcgagtggag tttccgatgt ttgagctctc 1140
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ctgttaaagt	tttgtgcatg	tcctctatat	gccaaatatt	tggtggttaag	cacgacaaag	1500
gtatgccaaa	tgaagttgta	ttaactatgt	tgaataagat	ggtcctatac	taatagatta	1560
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caagcagacc	catgccatat	ggcgtccatg	gggtagtcca	ggtgatattg	acgtaagttc	1680
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ggatatcccc	taagctattt	caaaaaatct	aggaacctta	tctgtagcag	actttgttaa	1860
tttttcaa	caagggactc	caacagccaa	gcgataaccc	tcaccaaatt	tgtgaaggat	1920
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tataaatttc	aatctcttaa	gtgtacacaa	aatacaagat	atttcactct	tttgtatttt	2100
tctaattccc	ataattttat	ctttattttg	tattttgatt	gaacccgagc	acatctttga	2160
cttgcaccaa	caatattagc	tctaaattaa	acatagaatt	taatgttaaa	atgagaaaag	2220
gaactcatac	agatcggact	caaaacctta	acaccttaata	aagtatgcat	cctaataaaa	2280
agttattacc	aaagtgaat	tatgcttaat	gaaaatcgaa	atcagaagta	gttcttaatt	2340
ggagagtttc	gagacggcaa	gaatattgca	actcatcctc	acacctaccc	atctatttca	2400
tactcttaaa	ttataatcta	attcaatata	cacaacaacc	tatcacatta	atatacaata	2460
tgaaaggtca	ataaaatatt	tacgctggca	aacctcccca	gtagaattcg	ggcacatatg	2520
aagtgttaac	cattcaaata	tggacaaagg	aacactagag	acacgaagtt	tatttcaaag	2580
gaaaattttg	tctaaaattg	aatttaatta	aatttaaatt	aattatataa	taaatataat	2640
gtattttaca	tcatgattga	tatataattt	taaaaaaaat	aattattcca	actattaaca	2700
ttaattaata	aataactttt	acaagacca	ggccaccaac	tcccgtccac	atgaaagaat	2760
gggtaaccgc	taagtctata	ttttagtact	acgacgtatg	caaatacgct	ttttccacaa	2820
aatcaaat	ttaattttta	ctttatccaa	ggcaagaaaa	caaaaaatgc	ataaattcac	2880
gttctaattc	atcaatactc	aagaaatagc	atacttgatt	tgaactgaga	tttgtcactt	2940
tcctacaaat	tctgcagact	atgaaaacga	catcaaccaa	ccaatatcca	ctctctatat	3000
aatagcatc	acttcactag	caattttctca	tcaactcata	gagtactcaa	aaacgctttt	3060
tcagccaac						3069

<210> 75

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, gSST-FW1

<400> 75

aatgaaattg acagatgacg tctagtgtgta

29

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, gSST-RV2

<400> 76

ctgcgaatta gaaagaattc tgtaaaccat

30

<210> 77
 <211> 2815
 <212> DNA
 <213> *Sesamum radiatum*

<400> 77
 tagtgtagtg tgaatgtgtg atatTTTTGc agtatatata ttgtaaaaga ggattaacca 60
 aatctctcta gtTCgtgatt atgactatTT ttgcagaaaa tttgtattta gtttaggggt 120
 ggtaaaatct aatttataga gtaaatatga tgtatttatt ttgtgattga ttacttttat 180
 atttattgta taattagtta taatttgata aagtgtgata ttttttataa attagattac 240
 atattattat gtactgagtt tttcgttctg atgccattta aaaattgggt aggtcggcga 300
 cttgaactga cgagtgaagg gacttgattt aacattttta ggatatatat atatatgacc 360
 agttatcaaa ataaaagttt tctttcaaaa tcatagtttt gtttaagata attttgtgag 420
 tatatgttgc accacaattc ccaagcacta taagtgcac tgtaggtcta attggacct 480
 gtttagttga caaaattgaa gtccaagaat atcttcaaga agccaattcg tgtaatggta 540
 cgtcaaaggt gccaccaggg aatcaagtag gaaatttccc ctaaattgta ggcatgaggt 600
 gccactataa agaaaattga cccaaagaga tacaagtatc ttagagtcga gaagaagact 660
 acgtagacca ttaggggaagt ccacatgcct aagattctgc agctgaagca caggcctagg 720
 tacggtcagc ccagggactc gagatccctc agctctcaaa gaattgggtat tggcccagga 780
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 tgaatcctat tttctcgggt gttcaaactc aagcatgtaa aataaataaa cgtgtgacta 900
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 cgtttgagct ttcgtcaatc cattcacgta gagataaacg gacgtctcct ctaagggtat 1020
 ccacaatacc attggcgagg agatttcttg tctattagag gattcgagat taccatggag 1080
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 aattctcaag ctttcaaacc tagttaaaag cttgagaaaa tttgtgcgta gatatgtttt 1200
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 aacaagatat tttactcatt tgttttctct tagttcctat aattttatct ttcttgcac 1920
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 gctcaagaaa tagcatactt gatttgaact gagatttgtc actatcctac aaattctgca 2700
 cactatgaaa acgacatcaa ccaacaaaaa tccactctct ataaatacca tcacttcaat 2760
 agcaatttct catcaactca taacgtactc aaataaacac gctttttcag ccaac 2815

<210> 78
 <211> 507
 <212> PRT
 <213> Sesumum alatum

<400> 78

Met	Glu	Ala	Glu	Met	Leu	Tyr	Ser	Ala	Leu	Ala	Leu	Thr	Phe	Ala	Ile
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Ile	Met	Val	His	Arg	Ile	Leu	Ser	Asn	Ser	Gln	Asn	Lys	Arg	Ser	Leu
			20					25					30		
Ile	Asn	Leu	Pro	Pro	Ser	Pro	Pro	Gly	Trp	Leu	Pro	Ile	Ile	Gly	His
		35					40					45			
Leu	His	Leu	Ile	Lys	Asn	Pro	Leu	His	Arg	Thr	Leu	Tyr	Asp	Cys	Ser
	50					55					60				
Gln	Lys	Leu	Gly	Ser	Ile	Phe	Ser	Val	Trp	Phe	Gly	Ser	Arg	Leu	Val
65					70					75					80
Val	Val	Val	Ser	Ser	Ser	Ser	Leu	Val	Glu	Glu	Cys	Phe	Thr	Lys	Tyr
				85					90					95	
Asp	Ile	Val	Leu	Ala	Asn	Arg	Pro	Asp	Leu	His	Leu	Asp	Leu	Arg	Ser
			100					105					110		
Leu	Gly	Ala	Ser	Thr	Ile	Ser	Val	Ile	Gly	Ala	Pro	Tyr	Gly	Asp	His
	115						120					125			
Trp	Arg	Asn	Leu	Arg	Lys	Leu	Cys	Asp	Leu	Glu	Val	Phe	Ala	Pro	Thr
	130					135					140				
Arg	Leu	Ala	Ser	Phe	Leu	Ser	Ile	Arg	Arg	Asp	Glu	Arg	Asp	Arg	Met
145					150					155					160
Ile	Ser	Gly	Leu	Tyr	Lys	Ile	Ser	Ser	Ala	Gly	Leu	Ala	Lys	Val	Asn
			165						170					175	
Leu	Glu	Ala	Lys	Ile	Ala	Glu	Leu	Thr	Phe	Asn	Asn	Leu	Met	Arg	Met
		180						185					190		
Leu	Ala	Gly	Lys	Ile	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Glu	Glu	Glu
	195						200					205			
Ala	Lys	Arg	Phe	Arg	Asp	Met	Thr	Lys	Glu	Ala	Leu	Glu	Leu	Met	Asn
	210					215					220				
Thr	Phe	Asn	Leu	Ala	Glu	Ile	Phe	Pro	Ile	Leu	Arg	Trp	Ile	Gly	Cys
225				230						235					240
Asn	Gly	Phe	Glu	Lys	Gln	Leu	Pro	Val	His	Ser	Arg	Lys	Thr	Asp	Glu
				245					250					255	
Ile	Met	Gln	Gly	Leu	Leu	Asp	Glu	His	Arg	Arg	Gly	Glu	Arg	Gln	Asn
			260					265					270		

Thr Met Val Gly His Leu Leu Ser Leu Gln Glu Ser Gln Pro Asp Tyr
 275 280 285
 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Ile Ser Leu Ile Ile Ala
 290 295 300
 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu
 305 310 315 320
 Leu Asn His Pro Lys Val Leu Glu Lys Ala Arg Gln Glu Met Asp Thr
 325 330 335
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 atgttcgtag ccggaacaga cacaactgca gctacaataa catgggcaat gacagctctg 960
 atcaagaagc ctcaagtact gaacaaagtg caacaagaaa tcagatctgt ggtcggaaaag 1020
 aaaggcagcg tagccgaaga tgatatacaa aaacttcctt attttaaagc ggtggtgaag 1080
 gagactctga gactgtacgc accagctcca ctctcactgc ccagactgac aatcaaaaagc 1140
 agcgtcatag atggatacga cattgaaccc aacaccatag ttacgtgaa cgtttgggcg 1200
 attagccgag acaaggattt ttgggagaac ccggatgagt tcttgcccga aagattcttg 1260
 aacagtagcg tggactttta aggccaagat ttcgggtttc ttccattcgg gtcggggcga 1320
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 ctgtattgct tccactggga attgccgcct ggaatggtag aagatgacgt tgatatggac 1440
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 ctg 1503

<210> 54
 <211> 501
 <212> PRT
 <213> Sesamum indicum

<220>

<223> SiP249

<400> 54

Met Ser Ile Pro Leu Leu Ile Ser Leu Ser Leu Ile Ile Leu Val Phe
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Leu Leu Val Arg Arg Arg Arg Asn Ser Pro Ala Gly Arg Lys Leu Arg
 20 25 30

Arg Pro Pro Gly Pro Pro Gly Leu Pro Phe Leu Gly Asn Leu Leu Gln
 35 40 45

Tyr Asn Pro Ser Asp Leu His Leu Arg Leu Thr Lys Leu Ser Glu Lys
 50 55 60

Tyr Gly Pro Leu Met Tyr Met Thr Phe Val Gly Lys Pro Val Val Val
 65 70 75 80

Ile Ser Ser Ala Arg Val Ala Lys Glu Ala Leu Lys Tyr Asn Asp Leu
 85 90 95

Ala Phe Ser Ser Arg Pro Ser Thr Ile Ala Ser Arg Lys Val Ala Tyr
 100 105 110

Asn Asn Ser Asp Ile Ser Met Ser Pro Tyr Thr Glu Tyr Trp Arg Glu
 115 120 125

Leu Arg Lys Met Val Val Leu Arg Leu Phe Thr Val Lys Gln Val Asn
 130 135 140

Ser Phe Arg Pro Ala Arg Glu Glu Glu Val Ala Arg Met Val Lys Glu
 145 150 155 160

Ile Ser Arg Arg Ala Asn Ala His Gln Pro Val Asn Ile Asn Glu Ile
 165 170 175

Ala Leu Ser Leu Ser Ser Arg Met Ile Ser Arg Phe Ala Leu Gly Lys
 180 185 190

Arg Tyr Asp Glu Glu Asn Gly Pro Glu Lys Arg Arg Phe Asp Arg Ile
 195 200 205

Leu Gln Leu Leu Gln Leu Val Ser Val Glu Ile Phe Phe Gly Asp Tyr
 210 215 220

Ser Pro Trp Leu Gly Trp Ile Asp Arg Leu Cys Gly Lys Val Ser Gln
 225 230 235 240

Leu Glu Lys Ala Phe Lys Asp Leu Asp Ser Leu Tyr Glu Glu Met Ile
 245 250 255

Ala Glu His Leu Ser Pro Asn Arg Pro Glu Ser Met Asn Gly Asp Ile
 260 265 270

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln
 275 280 285

Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala
 290 295 300
 Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu
 305 310 315 320
 Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser
 325 330 335
 Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu
 340 345 350
 Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro
 355 360 365
 Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp
 370 375 380
 Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala
 385 390 395 400
 Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro
 405 410 415
 Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly
 420 425 430
 Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu
 435 440 445
 Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe
 450 455 460
 His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp
 465 470 475 480
 Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met
 485 490 495
 Ala Lys Ser Tyr Leu
 500

<210> 55
 <211> 1545
 <212> DNA
 <213> Sesamum indicum

<220>
 <223> SiP288

<400> 55
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 cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccga 180
 cggggaactt ttcatttccg ggtcccttg ttggctgata tggacatgat ggggactgct 240
 gatcctgaga atgttacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300


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aagttcaggg aaatttttga tgttcttggga gatgggattt tcaatgcaga ttcggagtcc 360
tggagggacc agagaagggt tgccagggcc ctgatttctc accatgggtt cctccggtt 420
ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacggtg 480
tgcctggaag atcgggtgtt cgatttgcag gatttgttcc agaggttgac gtttgataca 540
acttgtacat ttgttactgg ttatgatcct ggatgcttgt ctgttgattt gcctgatgtt 600
cctttctcga aagccctaga tgaatgccga gaagcgatat tcatgcgcca tgtgttccct 660
gaaaagattt ggaaacttca gaggttggtt ggggttggat ctgagagaaa attgagcaag 720
gctcgtgaag tcttggatag cgtcattggc aggtataatc cgctgaagcg cggcgaagt 780
agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840
tacatgactg tgggagacga tgggtactcaa acccatgatt tgaaatgtga tgacaagttc 900
ttgagggaca cgatactgaa tctaatgatt gcagggcggg acacgacgag ttctgtctctg 960
acatggttta tatggcttgt gtcgacacat gctgaagtgg aaaagaggat cagggatgaa 1020
ctgaagtcct ttctgcccgc cggagaacgt gaaaagtggc gtgtgtttgg gtttgaagaa 1080
accaagaagt tggtttacat gcatggagca atttgcgaag ccttacgact atatccacca 1140
gtcccgttcc agcataagga gccggtggaa ccagatatcc ttccgagcgg gcattttgtg 1200
gaaccgacaa tgaaagtgat gttctcattg tacgcatagg gacggatgga atccgtttgg 1260
ggcgaggatt gcttgggaatt caagccggag aggtggattt ctgatagggg atcgatcaag 1320
cacgagccct catacaagtt cttggcttcc aatgctggtc cgaggacttg cttgggggaag 1380
gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440
cacgtggcag acggccaccg cgtgctgccc aattgttcca tcatcctcta catgaggaat 1500
ggattgaagg ttagggtgc caatagatgg tctgctaaga aaat 1545

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<210> 56

<211> 515

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP288

<400> 56

Met Val Gly Ile Val Tyr Ile Glu Leu Phe Leu Ser Val Met Trp Phe

1

Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp

20

25

30

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile

35

40

45

His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe

50

55

60

His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala

65

70

75

80

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe

85

90

95

Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly

100

105

110

Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala

115

120

125

Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile

130 135 140
 Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val
 145 150 155 160
 Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu
 165 170 175
 Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys
 180 185 190
 Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp
 195 200 205
 Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp
 210 215 220
 Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys
 225 230 235 240
 Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys
 245 250 255
 Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu
 260 265 270
 Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly
 275 280 285
 Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr
 290 295 300
 Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu
 305 310 315 320
 Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg
 325 330 335
 Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys
 340 345 350
 Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His
 355 360 365
 Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln
 370 375 380
 His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val
 385 390 395 400
 Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met
 405 410 415
 Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp
 420 425 430
 Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu

435 440 445
 Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe
 450 455 460
 Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val
 465 470 475 480
 His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu
 485 490 495
 Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala
 500 505 510
 Lys Lys Asn
 515

<210> 57

<211> 1494

<212> DNA

<213> Sesamum indicum

<220>

<223> SiP168

<400> 57

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 aaacctcttc ccataatcgg caacattctt gagcttgggt agaaacccca ccaatctctc 180
 gccaaactct ccaaaacctc cgggcccctg atgcgtctca agctgggaac catgacaaca 240
 gttgttgat cctcccggga aatctccagg atcgtgtctg aacaatatga ccaagttttc 300
 tccagccgaa cacacgcaga tgccatccga gcacttgacc accacaaaca ttccgtcgcc 360
 tggataccgg cggacaatca gtggcggaaa atccgtaaac tgtgcaaaga gaagatgttt 420
 tccggccaaa agcttgatgc gaaccagggc ctgaggaggg agaagttgcg taatttgcaa 480
 gactatgtga atgaatgctg cgttagtggc caggctgttg atattgggtg agctgccttt 540
 acgacgacc ttaatctgat atcgccact cttttctcgg tggattttgc tgattttggt 600
 tctggttcgt ctcaagagct taaggatgtt atgagcggga tagcgtctat catcgccga 660
 ccaaattttg ctgattgttt cctcttctt cggctggttg atccacaggg catcttccgc 720
 cagaccacgt tacatttcaa caagtgtttt aagatctttg atgaaattat cctgcaaagg 780
 ctacagacca atgattcggg gacgaaaagt gacatgctga aagagcttct tgaatcaac 840
 cagaaagatg agtctgaatt gagctttgac gagatcaagc atttactcct ggatctactt 900
 gtgcgaggaa cggacacaac ttccagttaca gtggaatggg caatgacgga gctagtgcgc 960
 caccctgaga aaatgtcgaa agccagaaat gagttaagaa atgtggtggg actgaataaa 1020
 gaaattcaag aatcagacat ctcaagactc ccttacctac gagcagtggg gaaagaaagt 1080
 ttcaggcttc accctgcaac tcccttatcg gtacctaca aggccgacga ggaagcagaa 1140
 atcaatggct atatatgcc taaaggagca caagttctca tgaacgtgtg ggccatcggc 1200
 agagattcaa gcataatggag gaacctgat gtaattcatgc ccgagaggtt cttggagaca 1260
 gaaattgatg tccgtggcca acacttcgag ctgcttccct ttggcggggg gaggaggatt 1320
 tgcgtggggc tgcgtagc ctatcgtatg atccatctcg tgcttgccac ttccataagc 1380
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 ttcgccctca ccctgcaaaa agccattcct ctcaaggcac ttccagttaa aatt 1494

<210> 58

<211> 498

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP168

<400> 58

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Ile Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys
 20 25 30

Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn
 35 40 45

Ile Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser
 50 55 60

Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr
 65 70 75 80

Val Val Val Ser Ser Pro Glu Ile Ser Arg Ile Val Leu Gln Gln Tyr
 85 90 95

Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu
 100 105 110

Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp
 115 120 125

Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys
 130 135 140

Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln
 145 150 155 160

Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly
 165 170 175

Val Ala Ala Phe Thr Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe
 180 185 190

Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys
 195 200 205

Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala
 210 215 220

Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg
 225 230 235 240

Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile
 245 250 255

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met
 260 265 270

Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser
 275 280 285
 Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr
 290 295 300
 Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg
 305 310 315 320
 His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val
 325 330 335
 Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr
 340 345 350
 Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro
 355 360 365
 Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr
 370 375 380
 Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly
 385 390 395 400
 Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg
 405 410 415
 Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu
 420 425 430
 Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr
 435 440 445
 Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp
 450 455 460
 Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys
 465 470 475 480
 Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val
 485 490 495
 Lys Ile

<210> 59
 <211> 1545
 <212> DNA
 <213> Sesamum indicum

<220>
 <223> SiP236

<400> 59
 atggcaaacc ccattgattt tctctcagc ccaacaccat atgtggctac aacccttctt 60
 tacgttctct tctctgttct tattgttaga ttcctcagca gaaagctgct cgggaagaag 120


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aggtaccatc ccattggtgg taccgtgttc aaccagctgc tgaacttcta taggttgcatt 180
gattatatgg ctgatcttgc aggggaagtac aagacttaca gactgattgc cccttttcgg 240
actgaggtct atacatctga ccccgctaata gttgagcaca tgttgaaaac gaatttcgaa 300
agttatggca agggacctta caattgcagc attctggggg atttgtttgg tgaaggaatt 360
ttcgcaatcg atggccataa gtggaggag cagagaaaag tgtcaagcct tgagttttct 420
acaagggttc tgagggatta cagtagcatc gtcttcagga aaaacgccgt aaggctcgca 480
aaaattctgt ctggagctgc aacttccaac caaccagtgg atattcaaga tcttttcatg 540
aaatcaactt ttgattctat ttcggaagtt gctttaggag ttgagcttga cagcttgggt 600
ggttcaaatg aagaagggtgc caaatttagc attgctgcag acgacgtgag tatgaggaca 660
ctttggagat acgtggatgt tctgtggaag ttaaagagag ctctaaatgt tggttcagaa 720
gcaaaactga agaaaagcct tcaagtgggt gatgaatttg tgtataagct gattcatagt 780
aggactcagc aaatgaacat gccaggaaat gattctgtta tgcagctgaa gaaagacgac 840
attttgtcaa gattcttgca acttactgag gccactccca agtacttgag ggacataaca 900
ataagcttta tagttgctgg taaagacaca acagcaacaa ctctctcctg gtttattttac 960
atgctttgca agtatcctca tgttcaggaa aagggtggagc aagagataaa agatgcgaca 1020
ggctgcaaaag aggtagcaga tatctcagaa ttttcagcct gtgtgacaga agaagctttg 1080
ggcaagatgc attatctcca tgcagcattg acagaaacac tgaggattta tccagcagtt 1140
gcggtggatg caaagcaatg tttgtgtgat gatataatgc cggatgggtt cagtgttaag 1200
aagggggaca tgggtggctta tcaaccatat gcaatgggaa ggatgaaatc catatggggt 1260
aatgatgcag aagagttcaa accagagaga tggcttgaca aaaacggttg cttccagcag 1320
gccagccctt ttaagtttac agctttccag gccggccctc gtctttgttt ggggaaagag 1380
tttgcttatac ggcagatgaa gatattctca gccattctgc tgagattctt taccatgaaa 1440
ctaagtgatg aaagaaagac agtaaaactac agaccaatgc tcactcttct catcgacggt 1500
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<210> 60

<211> 515

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP236

<400> 60

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Thr Thr Leu Leu Tyr Val Leu Phe Ser Val Leu Ile Val Arg Phe Leu
20 25 30

Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr
35 40 45

Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala
50 55 60

Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg
65 70 75 80

Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys
85 90 95

Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu
100 105 110

Gly Asp Leu Phe Gly Glu Gly-Ile Phe Ala Ile Asp Gly His Lys Trp

115 120 125
 Arg Glu Gln Arg Lys Val Ser Ser Leu Glu Phe Ser Thr Arg Val Leu
 130 135 140
 Arg Asp Tyr Ser Ser Ile Val Phe Arg Lys Asn Ala Val Arg Leu Ala
 145 150 155 160
 Lys Ile Leu Ser Gly Ala Ala Thr Ser Asn Gln Pro Val Asp Ile Gln
 165 170 175
 Asp Leu Phe Met Lys Ser Thr Phe Asp Ser Ile Ser Glu Val Ala Leu
 180 185 190
 Gly Val Glu Leu Asp Ser Leu Gly Gly Ser Asn Glu Glu Gly Ala Lys
 195 200 205
 Phe Ser Ile Ala Ala Asp Asp Val Ser Met Arg Thr Leu Trp Arg Tyr
 210 215 220
 Val Asp Val Leu Trp Lys Leu Lys Arg Ala Leu Asn Val Gly Ser Glu
 225 230 235 240
 Ala Lys Leu Lys Lys Ser Leu Gln Val Val Asp Glu Phe Val Tyr Lys
 245 250 255
 Leu Ile His Ser Arg Thr Gln Gln Met Asn Met Pro Gly Asn Asp Ser
 260 265 270
 Val Met Gln Leu Lys Lys Asp Asp Ile Leu Ser Arg Phe Leu Gln Leu
 275 280 285
 Thr Glu Ala Thr Pro Lys Tyr Leu Arg Asp Ile Thr Ile Ser Phe Ile
 290 295 300
 Val Ala Gly Lys Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Ile Tyr
 305 310 315 320
 Met Leu Cys Lys Tyr Pro His Val Gln Glu Lys Val Glu Gln Glu Ile
 325 330 335
 Lys Asp Ala Thr Gly Cys Lys Glu Val Ala Asp Ile Ser Glu Phe Ser
 340 345 350
 Ala Cys Val Thr Glu Glu Ala Leu Gly Lys Met His Tyr Leu His Ala
 355 360 365
 Ala Leu Thr Glu Thr Leu Arg Ile Tyr Pro Ala Val Ala Val Asp Ala
 370 375 380
 Lys Gln Cys Leu Cys Asp Asp Ile Met Pro Asp Gly Phe Ser Val Lys
 385 390 395 400
 Lys Gly Asp Met Val Ala Tyr Gln Pro Tyr Ala Met Gly Arg Met Lys
 405 410 415
 Ser Ile Trp Gly Asn Asp Ala Glu Glu Phe Lys Pro Glu Arg Trp Leu

420 425 430
 Asp Lys Asn Gly Cys Phe Gln Gln Ala Ser Pro Phe Lys Phe Thr Ala
 435 440 445
 Phe Gln Ala Gly Pro Arg Leu Cys Leu Gly Lys Glu Phe Ala Tyr Arg
 450 455 460
 Gln Met Lys Ile Phe Ser Ala Ile Leu Leu Arg Phe Phe Thr Met Lys
 465 470 475 480
 Leu Ser Asp Glu Arg Lys Thr Val Asn Tyr Arg Pro Met Leu Thr Leu
 485 490 495
 Leu Ile Asp Gly Gly Leu Ile Val Arg Pro Phe His Arg Met Asp Glu
 500 505 510
 Lys Thr Ala
 515

<210> 61

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, Bam-SST-FW2

<400> 61

tggatcccaa ctcatagagt actcaaaaac gctt

34

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, SiP189-Nco-RV

<400> 62

gcaaagatgc aaccatggtg ttct

24

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, GR-SST-RV1

<400> 63
cacatgaacg agacgaactg ggttttg 27

<210> 64
<211> 506
<212> PRT
<213> Sesamum radiatum

<220>
<223> SrSiP189

<400> 64
Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile
1 5 10 15

Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Glu Lys Ser Ser Leu
20 25 30

Ile Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His
35 40 45

Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser
50 55 60

Gln Lys Leu Gly Pro Ile Phe Ser Leu Arg Phe Gly Thr Arg Leu Val
65 70 75 80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr
85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser
100 105 110

Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His
115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr
130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met
145 150 155 160

Ile Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn
165 170 175

Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met
180 185 190

Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu
195 200 205

Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser
210 215 220

Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Phe
 225 230 235 240
 Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu
 245 250 255
 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn
 260 265 270
 Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr
 275 280 285
 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala
 290 295 300
 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile
 305 310 315 320
 Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr
 325 330 335
 Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu
 340 345 350
 Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser
 355 360 365
 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly
 370 375 380
 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala
 385 390 395 400
 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro
 405 410 415
 Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe
 420 425 430
 Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe
 435 440 445
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<210> 67
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18

<210> 68
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24

<210> 69
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Synthesized Primer Sequence, SiP189-nco-RV

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24

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<211> 25
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Synthesized Primer Sequence, STAR-LF1

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25

<210> 71
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Synthesized Primer Sequence, STAR-LR1

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<210> 72
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24

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<210> 76
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<212> DNA
<213> Artificial Sequence

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Synthesized Primer Sequence, gSST-RV2

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<210> 77

<211> 2815

<212> DNA

<213> *Sesamum radiatum*

<400> 177

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Leu His Leu Ile Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser
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Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val
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Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr
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Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser
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Leu Gly Ala Ser Thr Ile Ser Val Ile Gly Ala Pro Tyr Gly Asp His
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Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr
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